

0590
10/23

**RAW SEQUENCE LISTING
ERROR REPORT**

0590
0988

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/904994

Source: OIPE

Date Processed by STIC: 10/04/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER
VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/904994

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PT

1 _____ Wrapped Nucleics
_____ Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping"

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
_____ Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length.

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
_____ "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 ☒ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represent

10 _____ Invalid <213>
_____ Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
_____ "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001
TIME: 17:34:16

Input Set : A:\20005661.app
Output Set: N:\CRF3\10042001\I904994.raw

C--> 3 <110> APPLICANT: KUSTERS, Johannes G.
4 CATTOLI, Giovanni
6 <120> TITLE OF INVENTION: HELICOBACTER FELIS VACCINES
8 <130> FILE REFERENCE: KUSTERS
10 <140> CURRENT APPLICATION NUMBER: 09/904,994
11 <141> CURRENT FILING DATE: 2001-09-24
13 <150> PRIOR APPLICATION NUMBER: EP00202565.8
14 <151> PRIOR FILING DATE: 2000-07-17
16 <160> NUMBER OF SEQ ID NOS: 21
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2883
22 <212> TYPE: DNA
23 <213> ORGANISM: Helicobacter felis
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (206)..(886)
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (897)..(2603)
33 <400> SEQUENCE: 1
34 rggragattt tccarcactt caagcacata ttgatcctgt gttgtgggtg gtaaatttrcr 60
36 acttggttaat rctattatta attttttaat aattacttat tatcatatat aataatatta 120
38 ttactttatat taaaaagtta ataaaaagta acgaaattag gactataatc ccattgcctt 180
40 taaaatttaa cacaaggagt aatag gtg aaa ctc aca ccc aaa gag caa gaa 232
41 Val Lys Leu Thr Pro Lys Glu Gln Glu
42 1 5
44 aag ttc ttg tta tat tat gcg ggc gaa gtg gct aga aag cgc aaa gca 280
45 Lys Phe Leu Leu Tyr Tyr Ala Gly Glu Val Ala Arg Lys Arg Lys Ala
46 10 15 20 25
48 gag ggc tta aag ctc aac caa ccc gaa gcc att gct tac att agt gcc 328
49 Glu Gly Leu Lys Leu Asn Gln Pro Glu Ala Ile Ala Tyr Ile Ser Ala
50 30 35 40
52 cat att atg gac gaa gcg cgc cgt gga aaa aaa acc gtt gcc cag ctt 376
53 His Ile Met Asp Glu Ala Arg Arg Gly Lys Lys Thr Val Ala Gln Leu
54 45 50 55
56 atg gaa gag tgc atg cac ttt ttg aaa aaa gat gaa gta atg ccc ggg 424
57 Met Glu Glu Cys Met His Phe Leu Lys Lys Asp Glu Val Met Pro Gly
58 60 65 70
60 gtg ggt aat atg gtt ccc gat cta ggt gta gaa gcc acc ttt cct gat 472
61 Val Gly Asn Met Val Pro Asp Leu Gly Val Glu Ala Thr Phe Pro Asp
62 75 80 85
64 ggt acg aaa ctt gta act gtg aat tgg ccc atc gaa cca gat gag cac 520
65 Gly Thr Lys Leu Val Thr Val Asn Trp Pro Ile Glu Pro Asp Glu His
66 90 95 100 105
68 ttc aaa gcg ggc gaa gtg aaa ttt ggt tgc gat aaa gac atc gag ctc 568
69 Phe Lys Ala Gly Glu Val Lys Phe Gly Cys Asp Lys Asp Ile Glu Leu

Does Not Comply
Corrected Diskette Needed

See Page 6 of 8 A

*As well as Error
Summary Sheet*

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001

TIME: 17:34:16

Input Set : A:\20005661.app

Output Set: N:\CRF3\10042001\I904994.raw

```

70          110          115          120
72 aat gca ggc aaa gaa gta acc gaa ctt gag gtt act aat gaa ggg cct 616
73 Asn Ala Gly Lys Glu Val Thr Glu Leu Glu Val Thr Asn Glu Gly Pro
74          125          130          135
76 aaa tcc ttg cat gtg ggt agc cat ttc cac ttc ttt gaa gct aac aag 664
77 Lys Ser Leu His Val Gly Ser His Phe His Phe Phe Glu Ala Asn Lys
78          140          145          150
80 gca cta aaa ttc gat cgt gaa aaa gcc tat ggc aaa cgc cta gat att 712
81 Ala Leu Lys Phe Asp Arg Glu Lys Ala Tyr Gly Lys Arg Leu Asp Ile
82          155          160          165
84 ccc tct ggc aac acg cta cgc att ggg gca gga caa acc cgc aaa gtg 760
85 Pro Ser Gly Asn Thr Leu Arg Ile Gly Ala Gly Gln Thr Arg Lys Val
86 170          175          180          185
88 cag ttg att cct ctt ggt ggc agt aaa aaa gtg att ggc atg aac ggg 808
89 Gln Leu Ile Pro Leu Gly Gly Ser Lys Lys Val Ile Gly Met Asn Gly
90          190          195          200
92 ctt gtg aat aac atc gcg gat gaa cgc cat aaa cat aaa gcg ctt gac 856
93 Leu Val Asn Asn Ile Ala Asp Glu Arg His Lys His Lys Ala Leu Asp
94          205          210          215
96 aag gcg aaa tct cac gga ttt atc aag taa ggagactccc atg aaa atg 905
97 Lys Ala Lys Ser His Gly Phe Ile Lys          Met Lys Met
W--> 98          220          225          230 OK
100 aaa aaa caa gaa tat gta aat acc tac gga ccc acc aaa ggc gat aaa 953
101 Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Lys Gly Asp Lys
W--> 102          235          240          245
104 gtg cgc tta gga gat acc gat ctt tgg gca gaa gta gaa cat gac tat 1001
105 Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu His Asp Tyr
W--> 106          250          255          260
108 acc acc tat ggc gaa gaa ctt aaa ttt ggc gcg ggt aaa act atc cgt 1049
109 Thr Thr Tyr Gly Glu Glu Leu Lys Phe Gly Ala Gly Lys Thr Ile Arg
W--> 110          265          270          275
112 gag ggt atg ggt cag agc aat agc cct gat gaa aac acc cta gat tta 1097
113 Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr Leu Asp Leu
W--> 114          280          285          290
116 gtc atc act aac gcg atg att atc gac tac acc ggg att tac aaa gcc 1145
117 Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile Tyr Lys Ala
W--> 118 295          300          305          310
120 gac att ggg att aaa aac ggc aaa atc cat ggc att ggc aag gca gga 1193
121 Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly Lys Ala Gly
W--> 122          315          320          325
124 aac aag gac atg caa gat ggc gta agc cct cat atg gtc gtg ggt gtg 1241
125 Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val Val Gly Val
W--> 126          330          335          340
128 ggc aca gaa gca cta gca ggg gaa ggt atg att att acc gct ggg gga 1289
129 Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr Ala Gly Gly
W--> 130          345          350          355
132 atc gat tca cac acc cac ttc ctt tct cca caa caa ttc cct acc gct 1337
133 Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe Pro Thr Ala
W--> 134          360          365          370

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Input Set : A:\20005661.app

Output Set: N:\CRF3\10042001\I904994.raw

```

136 cta gcc aat ggc gtt aca acc atg ttt gga ggc ggc aca ggt cct gta 1385
137 Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr Gly Pro Val
W--> 138 375          380          385          390
140 gat ggc acg aat gcg act act atc act ccg ggc aaa tgg aac ttg cac 1433
141 Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp Asn Leu His
W--> 142          395          400          405
144 cgc atg ttg cgc gca gca gaa gag tat tct atg aat gtg ggc ttt ttg 1481
145 Arg Met Leu Arg Ala Ala Glu Glu Tyr Ser Met Asn Val Gly Phe Leu
W--> 146          410          415          420
148 ggc aaa ggc aat agc tct agc aaa aaa caa ctt gta gaa caa gta gaa 1529
149 Gly Lys Gly Asn Ser Ser Ser Lys Lys Gln Leu Val Glu Gln Val Glu
W--> 150          425          430          435
152 gcg ggc gcg att ggt ttt aaa ttg cat gaa gac tgg ggc aca aca cca 1577
153 Ala Gly Ala Ile Gly Phe Lys Leu His Glu Asp Trp Gly Thr Thr Pro
W--> 154          440          445          450
156 agt gcg atc gat cac tgc ttg agc gtg gca gat gaa tac gat gtg caa 1625
157 Ser Ala Ile Asp His Cys Leu Ser Val Ala Asp Glu Tyr Asp Val Gln
W--> 158 455          460          465          470
160 gtt tgt atc cac acc gat aca gtc aat gag gca ggt tat gta gat gac 1673
161 Val Cys Ile His Thr Asp Thr Val Asn Glu Ala Gly Tyr Val Asp Asp
W--> 162          475          480          485
164 acc cta aat gca atg aac ggg cgc gcc atc cat gcc tac cac att gag 1721
165 Thr Leu Asn Ala Met Asn Gly Arg Ala Ile His Ala Tyr His Ile Glu
W--> 166          490          495          500
168 gga gcg ggt gga gga cac tca cct gat gtt atc acc atg gca ggc gag 1769
169 Gly Ala Gly Gly Gly His Ser Pro Asp Val Ile Thr Met Ala Gly Glu
W--> 170          505          510          515
172 ctc aat att cta ccc tcc tcc acc acc ccc act att ccc tat acc att 1817
173 Leu Asn Ile Leu Pro Ser Ser Thr Thr Pro Thr Ile Pro Tyr Thr Ile
W--> 174          520          525          530
176 aat acg gtt gca gaa cac tta gac atg ctc atg aca tgc cac cac cta 1865
177 Asn Thr Val Ala Glu His Leu Asp Met Leu Met Thr Cys His His Leu
W--> 178 535          540          545          550
180 gac aaa cgc atc cgc gag gat tta caa ttt tct caa agc cgt atc cgc 1913
181 Asp Lys Arg Ile Arg Glu Asp Leu Gln Phe Ser Gln Ser Arg Ile Arg
W--> 182          555          560          565
184 ccc ggc tct atc gcg gct gaa gat gtg ctc cat gat atg ggt gtg atc 1961
185 Pro Gly Ser Ile Ala Ala Glu Asp Val Leu His Asp Met Gly Val Ile
W--> 186          570          575          580
188 gcg atg aca agc tcg gat tcg caa gca atg ggg cgt gca ggc gaa gtg 2009
189 Ala Met Thr Ser Ser Asp Ser Gln Ala Met Gly Arg Ala Gly Glu Val
W--> 190          585          590          595
192 att cct cga act tgg cag act gcg gat aag aat aaa aaa gaa ttt ggt 2057
193 Ile Pro Arg Thr Trp Gln Thr Ala Asp Lys Asn Lys Lys Glu Phe Gly
W--> 194          600          605          610
196 aag ctt cct gaa gat ggc aaa gat aac gat aat ttc cgc att aag cgc 2105
197 Lys Leu Pro Glu Asp Gly Lys Asp Asn Asp Asn Phe Arg Ile Lys Arg
W--> 198 615          620          625          630
200 tac atc tcc aaa tac act atc aac ccc gct ttg acc cac ggc gtg agc 2153

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/904,994

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Input Set : A:\20005661.app

Output Set: N:\CRF3\10042001\I904994.raw

```

201 Tyr Ile Ser Lys Tyr Thr Ile Asn Pro Ala Leu Thr His Gly Val Ser
W--> 202          635          640          645
204 gag tat atc ggc tct gtg gaa gag ggc aag atc gcc gac ttg gtg gtg 2201
205 Glu Tyr Ile Gly Ser Val Glu Glu Gly Lys Ile Ala Asp Leu Val Val
W--> 206          650          655          660
208 tgg aat cct gcc ttt ttt ggc gta aaa ccc aaa atc gtg atc aaa ggc 2249
209 Trp Asn Pro Ala Phe Phe Gly Val Lys Pro Lys Ile Val Ile Lys Gly
W--> 210          665          670          675
212 ggt atg gtg gtc ttc tct gaa atg ggc gat tct aac gcg tct gtg ccc 2297
213 Gly Met Val Val Phe Ser Glu Met Gly Asp Ser Asn Ala Ser Val Pro
W--> 214          680          685          690
216 act ccc caa ccg gtt tat tac cgc gaa atg ttt ggg cat cac ggc aag 2345
217 Thr Pro Gln Pro Val Tyr Tyr Arg Glu Met Phe Gly His His Gly Lys
W--> 218 695          700          705          710
220 gcg aaa ttt gac acc agc atc act ttt gtt tcc aaa gtc gcc tat gaa 2393
221 Ala Lys Phe Asp Thr Ser Ile Thr Phe Val Ser Lys Val Ala Tyr Glu
W--> 222          715          720          725
224 aat ggc gtg aaa gaa aag ctg ggc tta gag cgc caa gtt cta ccg gtc 2441
225 Asn Gly Val Lys Glu Lys Leu Gly Leu Glu Arg Gln Val Leu Pro Val
W--> 226          730          735          740
228 aaa aac tgc cgt aac atc acc aag aaa gac ttc aag ttc aac gac aaa 2489
229 Lys Asn Cys Arg Asn Ile Thr Lys Lys Asp Phe Lys Phe Asn Asp Lys
W--> 230          745          750          755
232 acg gca aaa atc acc gtc gat ccg aaa acc ttc gag gtc ttt gta gat 2537
233 Thr Ala Lys Ile Thr Val Asp Pro Lys Thr Phe Glu Val Phe Val Asp
W--> 234          760          765          770
236 ggc aaa ctc tgc acc tct aaa ccc acc tcg caa gtg cct cta gcc cag 2585
237 Gly Lys Leu Cys Thr Ser Lys Pro Thr Ser Gln Val Pro Leu Ala Gln
W--> 238 775          780          785          790
240 cgc tac act ttc ttc tag gcacaatgcc ccctttgggg gcaggttatt 2633
241 Arg Tyr Thr Phe Phe
W--> 242          795
244 tttaggaatct tcatcaaacy cacctgcaat cgggtcttgcg tgtgcgatcg tgtcgcttta 2693
246 aaacaacttt tcatctttaa gcaatcgcca tttttaatta atttaattct tataattaat 2753
248 attatattat gcccctcat ttttaaagga gaattatgcy taggtctttg gtattgctat 2813
250 gtggggggtt tttggtgctg ggcgcgaaagg gtattgaaac ccatcgctc aaaaaagtag 2873
252 aagccacagg 2883
255 <210> SEQ ID NO: 2
256 <211> LENGTH: 226
257 <212> TYPE: PRT
258 <213> ORGANISM: Helicobacter felis
260 <400> SEQUENCE: 2
261 Val Lys Leu Thr Pro Lys Glu Gln Glu Lys Phe Leu Leu Tyr Tyr Ala
262 1 5 10 15
263 Gly Glu Val Ala Arg Lys Arg Lys Ala Glu Gly Leu Lys Leu Asn Gln
264 20 25 30
265 Pro Glu Ala Ile Ala Tyr Ile Ser Ala His Ile Met Asp Glu Ala Arg
266 35 40 45
267 Arg Gly Lys Lys Thr Val Ala Gln Leu Met Glu Glu Cys Met His Phe

```

RAW SEQUENCE LISTING

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DATE: 10/04/2001

TIME: 17:34:16

Input Set : A:\20005661.app

Output Set: N:\CRF3\10042001\I904994.raw

```

268      50      55      60
269 Leu Lys Lys Asp Glu Val Met Pro Gly Val Gly Asn Met Val Pro Asp
270 65      70      75      80
271 Leu Gly Val Glu Ala Thr Phe Pro Asp Gly Thr Lys Leu Val Thr Val
272      85      90      95
273 Asn Trp Pro Ile Glu Pro Asp Glu His Phe Lys Ala Gly Glu Val Lys
274      100      105      110
275 Phe Gly Cys Asp Lys Asp Ile Glu Leu Asn Ala Gly Lys Glu Val Thr
276      115      120      125
277 Glu Leu Glu Val Thr Asn Glu Gly Pro Lys Ser Leu His Val Gly Ser
278      130      135      140
279 His Phe His Phe Phe Glu Ala Asn Lys Ala Leu Lys Phe Asp Arg Glu
280 145      150      155      160
281 Lys Ala Tyr Gly Lys Arg Leu Asp Ile Pro Ser Gly Asn Thr Leu Arg
282      165      170      175
283 Ile Gly Ala Gly Gln Thr Arg Lys Val Gln Leu Ile Pro Leu Gly Gly
284      180      185      190
285 Ser Lys Lys Val Ile Gly Met Asn Gly Leu Val Asn Asn Ile Ala Asp
286      195      200      205
287 Glu Arg His Lys His Lys Ala Leu Asp Lys Ala Lys Ser His Gly Phe
288      210      215      220
289 Ile Lys
290 225
293 <210> SEQ ID NO: 3
294 <211> LENGTH: 568
295 <212> TYPE: PRT
296 <213> ORGANISM: Helicobacter felis
298 <400> SEQUENCE: 3
299 Met Lys Met Lys Lys Gln Glu Tyr Val Asn Thr Tyr Gly Pro Thr Lys
300 1      5      10      15
301 Gly Asp Lys Val Arg Leu Gly Asp Thr Asp Leu Trp Ala Glu Val Glu
302      20      25      30
303 His Asp Tyr Thr Thr Tyr Gly Glu Leu Lys Phe Gly Ala Gly Lys
304      35      40      45
305 Thr Ile Arg Glu Gly Met Gly Gln Ser Asn Ser Pro Asp Glu Asn Thr
306      50      55      60
307 Leu Asp Leu Val Ile Thr Asn Ala Met Ile Ile Asp Tyr Thr Gly Ile
308 65      70      75      80
309 Tyr Lys Ala Asp Ile Gly Ile Lys Asn Gly Lys Ile His Gly Ile Gly
310      85      90      95
311 Lys Ala Gly Asn Lys Asp Met Gln Asp Gly Val Ser Pro His Met Val
312      100      105      110
313 Val Gly Val Gly Thr Glu Ala Leu Ala Gly Glu Gly Met Ile Ile Thr
314      115      120      125
315 Ala Gly Gly Ile Asp Ser His Thr His Phe Leu Ser Pro Gln Gln Phe
316      130      135      140
317 Pro Thr Ala Leu Ala Asn Gly Val Thr Thr Met Phe Gly Gly Gly Thr
318 145      150      155      160
319 Gly Pro Val Asp Gly Thr Asn Ala Thr Thr Ile Thr Pro Gly Lys Trp

```

210> 10
 <211> 2407
 <212> DNA
 <213> Helicobacter felis

<220>
 <221> CDS
 <222> (2)..(682)

<220>
 <221> CDS
 <222> (693)..(2399)

<400> 10

ccc gcc tct gaa gtg cct cta gcc cag cgc tac act ttc ttc tag	2399
Pro Ala Ser Glu Val Pro Leu Ala Gln Arg Tyr Thr Phe Phe	
785 790 795	

gcncaatg 2407

<210> 11
 <211> 226
 <212> PRT
 <213> Helicobacter felis

Errored: As you can see sequence 10 includes
 sequence 10 includes unknown nucleotides. It
 is required that you describe unknowns in fields
 221, 222 and 223.

may
 The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001

TIME: 17:34:17

Input Set : A:\20005661.app

Output Set: N:\CRF3\10042001\I904994.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:110 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:130 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:158 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:162 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:174 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:186 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:194 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:198 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:202 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:206 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:214 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:222 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:226 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:234 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:238 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:242 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:446 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:450 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:454 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:458 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:462 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:466 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:470 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:474 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:478 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:482 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/904,994

DATE: 10/04/2001

TIME: 17:34:17

Input Set : A:\20005661.app

Output Set: N:\CRF3\10042001\I904994.raw

L:486 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:1232 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:1232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10